1 GGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT
51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GAACTGGCTT
101 CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG
151 GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA
201 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG
251 GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA
301 CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA
351 CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG
401 GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC
451 GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCCTGTC
501 GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GCTCGTCAGG
551 GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCCGAATTA CCGCGGTCTT
601 TCTCAACGTA ACACTTTACA GCGGCGCGTC ATTTGATATG ATGCGCCCCG
651 CTTCCCGATA AGGGAGCAGG CCAGTAAAAG CATTACCCGT GGTGGGGTTC
701 CCGAGCGGCC AAAGGGAGCA GACTCTAAAT CTGCCGTCAT CGACTTCGAA
751 GGTTCGAATC CTTCCCCCAC CACCATCACT TTCAAAAGTC CGAAAGAATC
801 TGCTCCCTGC TTGTGTGTTG GAGGTCGCTG AGTAGTGCGC GAGTAAAATT
851 TAAGCTACAA CAAGGCAAGG CTTGACCGAC AATTGCATGA AGAATCTGCT
901 TAGGGTTAGG CGTTTTGCGC TGCTTCGCGA TGTACGGGCC AGATATACGC
951 GTTGACATTG ATTATTGACT AGTTATTAAT AGTAATCAAT TACGGGGTCA
1001 TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC TTACGGTAAA
1051 TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG ACGTCAATAA
1101 TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA
1151 TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA
1201 TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG
1251 CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG
1301 TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC GGTTTTGGCA
1351 GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC
1401 TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG
1451 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG
1501 AATTCCTGGG CGGGACTGGG GAGTGGCGAG CCCTCAGATG CTGCATATAA
1551 GCAGCTGCTT TTTGCCTGTA CTGGGTCTCT CTGGTTAGAC CAGATCTGAG
1601 CCTGGGAGCT CTCTGGCTAA CTAGAGAACC CACTGCTTAA GCCTCAATAA
1651 AGCTTCTAGA GATCCCTCGA CCTCGAGGGA TCTTCCATAC CTACCAGTTC

FIG. 1-1

1701 TGCGCCTGCA GGTCGCGGCC GCGACTCTAG AGGATCTTTG TGAAGGAACC
1751 TTACTTCTGT GGTGTGACAT AATTGGACAA ACTACCTACA GAGATTTAAA
1801 GCTCTAAGGT AAATATAAAA TTTTTAAGTG TATAATGTGT TAAACTACTG
1851 ATTCTAATTG TTTGTGTATT TTAGATTCCA ACCTATGGAA CTGATGAATG
1901 GGAGCAGTGG TGGAATGCCT TTAATGAGGA AAACCTGTTT TGCTCAGAAG
1951 AAATGCCATC TAGTGATGAT GAGGCTACTG CTGACTCTCA ACATTCTACT
2001 CCTCCAAAAA AGAAGAGAAA GGTAGAAGAC CCCAAGGACT TTCCTTCAGA
2051 ATTGCTAAGT TTTTTGAGTC ATGCTGTGTT TAGTAATAGA ACTCTTGCTT
2101 GCTTTGCTAT TTACACCACA AAGGAAAAAG CTGCACTGCT ATACAAGAAA
2151 ATTATGGAAA AATATTCTGT AACCTTTATA AGTAGGCATA ACAGTTATAA
2201 TCATAACATA CTGTTTTTTC TTACTCCACA CAGGCATAGA GTGTCTGCTA
2251 TTAATAACTA TGCTCAAAAA TTGTGTACCT TTAGCTTTTT AATTTGTAAA
2301 GGGGTTAATA AGGAATATTT GATGTATAGT GCCTTGACTA GAGATCATAA
2351 TCAGCCATAC CACATTTGTA GAGGTTTTAC TTGCTTTAAA AAACCTCCCA
2401 CACCTCCCCC TGAACCTGAA ACATAAAATG AATGCAATTG TTGTTGTTAA
2451 CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT AGCATCACAA
2501 ATTTCACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTCC
2551 AAACTCATCA ATGTATCTTA TCATGTCTGG ATCCTGTGGA ATGTGTGTCA
2601 GTTAGGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA
2651 GCATGCATCT CAATTAGTCA GCAACCAGGT GTGGAAAGTC CCCAGGCTCC
2701 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAT
2751 AGTCCCGCCC CTAACTCCGC CCATCCCGCC CCTAACTCCG CCCAGTTCCG
2801 CCCATTCTCC GCCCCATGGC TGACTAATTT TTTTTATTTA TGCAGAGGCC
2851 GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG GAGGCTTTTT
2901 TGGAGGCCTA GGCTTTTGCA AAAAGCTAAT TC

FIG. 1-2

```
                CCTAAGATGAGCTTTCCATGTAAATTTGTAGCCAGCTTCCTTCTGATTTTCAATGTTTCT   (60)
                    METSERPHEPROCYSLYSPHEVALALASERPHELEULEUILEPHEASNVALSER

                TCCAAAGGTGCAGTCTCCAAAGAGATTACGAATGCCTTGGAAACCTGGGGTGCCTTGGGT  (120)
                SERLYSGLYALAVALSERLYSGLUILETHRASNALALEUGLUTHRTRPGLYALALEUGLY
                1
                CAGGACATCAACTTGGACATTCCTAGTTTTCAAATGAGTGATGATATTGACGATATAAAA  (180)
20              GLNASPILEASNLEUASPILEPROSERPHEGLNMETSERASPASPILEASPASPILELYS

                TGGGAAAAAAACTTCAGACAAGAAAAAAGATTGCACAATTCAGAAAAGAGAAAGAGACTTTC  (240)
40              TRPGLULYSTHRSERASPLYSLYSLYSILEALAGLNPHEARGLYSGLULYSGLUTHRPHE

                AAGGAAAAAAGATACATATAAGCTATTTAAAAATGGAACTCTGAAAATTAAGCATCTGAAG  (300)
60              LYSGLULYSASPTHRTYRLYSLEUPHELYSASNGLYTHRLEULYSILELYSHISLEULYS
                                                  ---CHO---
                ACCGATGATCAGGATATCTACAAGGTATCAATATATGATACAAAAGGAAAAAAATGTGTTG  (360)
80              THRASPASPGLNASPILETYRLYSVALSERILETYRASPTHRLYSGLYLYSASNVALLEU

                GAAAAAATATTTGATTTGAAGATTCAAGAGAGGGTCTCAAAACCAAAGATCTCCTGGACT  (420)
100             GLULYSILEPHEASPLEULYSILEGLNGLUARGVALSERLYSPROLYSILESERTRPTHR

                TGTATCAACACAACCCTGACCTGTGAGGTAATGAATGGAACTGACCCCGAATTAAACCTG  (480)
120             CYSILEASNTHRTHRLEUTHRCYSGLUVALMETASNGLYTHRASPPROGLULEUASNLEU
                   ---CHO---                      ---CHO---
                TATCAAGATGGGAAACATCTAAAACTTTCTCAGAGGGTCATCACACACAAGTGGACCACC  (540)
140             TYRGLNASPGLYLYSHISLEULYSLEUSERGLNARGVALILETHRHISLYSTRPTHRTHR

                AGCCTGAGTGCAAAATTCAAGTGCACAGCAGGGAACAAAGTCAGCAAGGAATCCAGTGTC  (600)
160             SERLEUSERALALYSPHELYSCYSTHRALAGLYASNLYSVALSERLYSGLUSERSERVAL

                GAGCCTGTCAGCTGTCCAGAGAAAGGTCTGGACATCTATCTCATCATTGGCATATGTGGA  (660)
180             GLUPROVALSERCYSPROGLULYSGLYLEUASPILETYRLEUILEILEGLYILECYSGLY
                                                  ------------------------
                GGAGGCAGCCTCTTGATGGTCTTTGTGGCACTGCTCGTTTTCTATATCACCAAAAGGAAA  (720)
200             GLYGLYSERLEULEUMETVALPHEVALALALEULEUVALPHETYRILETHRLYSARGLYS
                ----------TM-------------------------------------
                AAACAGAGGAGTCGGAGAAATGATGAGGAGCTGGAGACAAGAGCCCACAGAGTAGCTACT  (780)
220             LYSGLNARGSERARGARGASNASPGLUGLULEUGLUTHRARGALAHISARGVALALATHR

                GAAGAAAGGGGCCGGAAGCCCCAACAAATTCCAGCTTCAACCCCTCAGAATCCAGCAACT  (840)
240             GLUGLUARGGLYARGLYSPROGLNGLNILEPROALASERTHRPROGLNASNPROALATHR

                TCCCAACATCCTCCTCCACCACCTGGTCATCGTTCCCAGGCACCTAGTCATCGTCCCCCG  (900)
260             SERGLNHISPROPROPROPROPROGLYHISARGSERGLNALAPROSERHISARGPROPRO

                CCTCCTGGACACCGTGTTCAGCACCAGCCTCAGAAGAGGCCTCCTGCTCCGTCGGGCACA  (960)
280             PROPROGLYHISARGVALGLNHISGLNPROGLNLYSARGPROPROALAPROSERGLYTHR
```

FIG. 2-1

CAAGTTCACCAGCAGAAAGGCCCGCCCCTCCCCAGACCTCGAGTTCAGCCAAAACCTCCC (1020)
300 GlnValHisGlnGlnLysGlyProProLeuProArgProArgValGlnProLysProPro

CATGGGGCAGCAGAAAACTCATTGTCCCCTTCCTCTAATTAAAAAAGATAGAAACTGTCT (1080)
320 HisGlyAlaAlaGluAsnSerLeuSerProSerSerAsnEnd

TTTTCAATAAAAAGCACTGTGGATTTCTGCCCTCCTGATGTGCATATCCGTACTTCCATG (1140)

AGGTGTTTTCTGTGTGCAGAACATTGTCACCTCCTGAGGCTGTGGCCACAGCCACCTCT (1200)

GCATCTTCGAACTCAGCCATGTGGTCAACATCTGGAGTTTTTGGTCTCCTCAGAGAGCTC (1260)

CATCACACCAGTAAGGAGAAGCAATATAAGTGTGATTGCAAGAATGGTAGAGGACCGAGC (1320)

ACAGAAATCTTAGAGATTTCTTGTCCCCTCTCAGGTCATGTGTAGATGCGATAAATCAAG (1380)

TGATTGGTGTGCCTGGGTCTCACTACAAGCAGCCTATCTGCTTAAGAGACTCTGGAGTTT (1440)

CTTATGTGCCCTGGTGGACACTTGCCCACCATCCTGTGAGTAAAAGTGAAATAAAAGCTT (1500)

TGAC (1504)

FIG. 2-2

```
1 GCCCGACGAGCCATGGTTGCTGGGAGCGACGCGGGGCGGGCCCTGGGGGTCCTCAGCGTGGTCTGCCTGCTGCACTGCTTTGGTTTCATC 90
1              MetValAlaGlySerAspAlaGlyArgAlaLeuGlyValLeuSerValValCysLeuLeuHisCysPheGlyPheIle 26

91 AGCTGTTTTTCCCAACAAATATATGGTGTTGTGTATGGGAATGTAACTTTCCATGTACCAAGCAATGTGCCTTTAAAAGAGGTCCTATGG 180
27 SerCysPheSerGlnGlnIleTyrGlyValValTyrGlyAsnValThrPheHisValProSerAsnValProLeuLysGluValLeuTrp 56
                                    ---CHO---

181 AAAAAACAAAAGGATAAAGTTGCAGAACTGGAAAATTCTGAATTCAGAGCTTTCTCATCTTTTAAAAATAGGGTTTATTTAGACACTGTG 270
57 LysLysGlnLysAspLysValAlaGluLeuGluAsnSerGluPheArgAlaPheSerSerPheLysAsnArgValTyrLeuAspThrVal 86

271 TCAGGTAGCCTCACTATCTACAACTTAACATCATCAGATGAAGATGAGTATGAAATGGAATCGCCAAATATTACTGATACCATGAAGTTC 360
87 SerGlySerLeuThrIleTyrAsnLeuThrSerSerAspGluAspGluTyrGluMetGluSerProAsnIleThrAspThrMetLysPhe 116
                  ---CHO---                                                    ---CHO---

361 TTTCTTTATGTGCTTGAGTCTCTTCCATCTCCCACACTAACTTGTGCATTGACTAATGGAAGCATTGAAGTCCAATGCATGATACCAGAG 450
117 PheLeuTyrValLeuGluSerLeuProSerProThrLeuThrCysAlaLeuThrAsnGlySerIleGluValGlnCysMetIleProGlu 146
                                                  ---CHO---

451 CATTACAACAGCCATCGAGGACTTATAATGTACTCATGGGATTGTCCTATGGAGCAATGTAAACGTAACTCAACCAGTATATATTTTAAG 540
147 HisTyrAsnSerHisArgGlyLeuIleMetTyrSerTrpAspCysProMetGluGlnCysLysArgAsnSerThrSerIleTyrPheLys 176
                                                                    ---CHO---

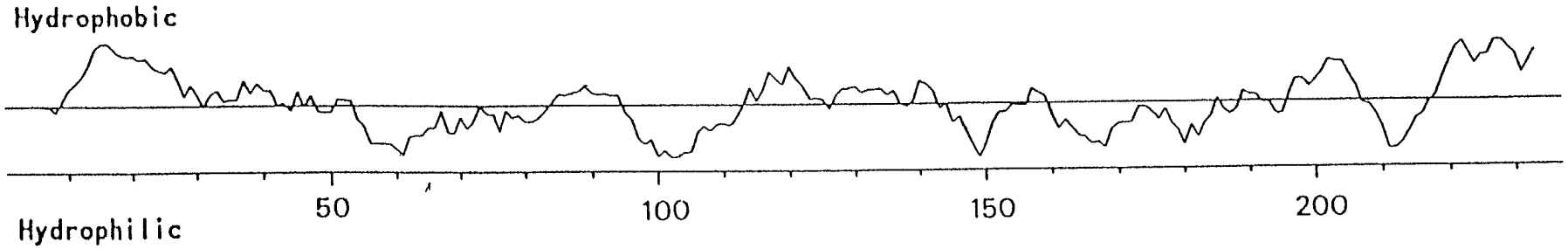
541 ATGGAAAATGATCTTCCACAAAAAATACAGTGTACTCTTAGCAATCCATTATTTAATACAACATCATCAATCATTTTGACAACCTGTATC 630
177 MetGluAsnAspLeuProGlnLysIleGlnCysThrLeuSerAsnProLeuPheAsnThrThrSerSerIleIleLeuThrThrCysIle 206
                                                ---CHO---

631 CCAAGCAGCGGTCATTCAAGACACAGATATGCACTTATACCCATACCATTAGCAGTAATTACAACATGTATTGTGCTGTATATGAATGTT 720
207 ProSerSerGlyHisSerArgHisArgTyrAlaLeuIleProIleProLeuAlaValIleThrThrCysIleValLeuTyrMetAsnVal 236
                                    ==========

721 CTTTAATTGAGAAGACAATTTCTTCATTTTTAGGTATTCTGAAATGTGACAGAAAACCAGACAGAACCAACTCCAATTGATTGGTAACAG 810
237 LeuEnd
    ===
811 AAGATGAAGACAACAGCATAACTAAATTATTTTAAAAACTAAAAAGCCATCTGATTTCTCATTT 874
```

FIG. 4A

FIG. 4B



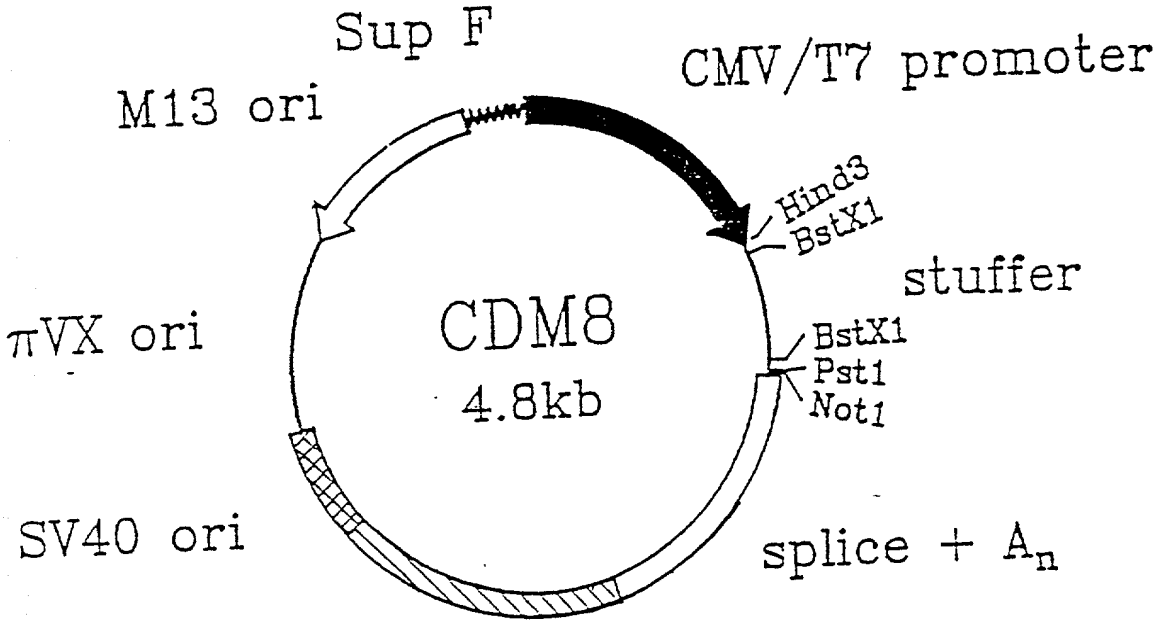

Sup F
CMV/T7 promoter
M13 ori
Hind3
BstX1
stuffer
πVX ori
CDM8
4.8kb
BstX1
Pst1
Not1
SV40 ori
splice + An
Py ori

FIG. 3

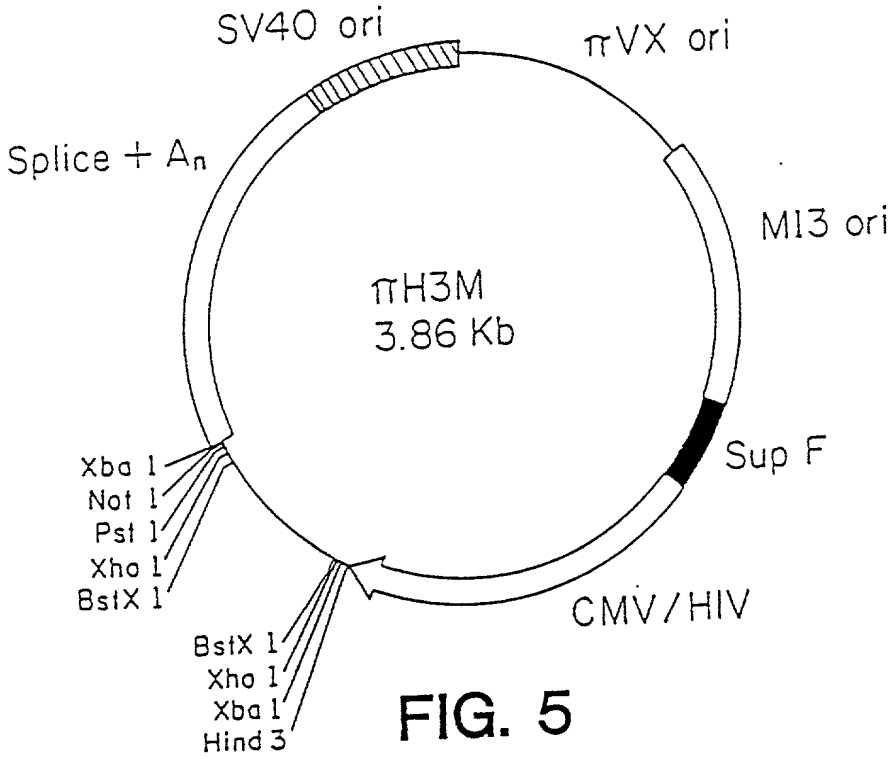

SV40 ori
πVX ori
Splice + An
MI3 ori
πH3M
3.86 Kb
Sup F
Xba 1
Not 1
Pst 1
Xho 1
BstX 1
CMV/HIV
BstX 1
Xho 1
Xba 1
Hind 3

FIG. 5

1 GGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT

51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT

101 TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA

151 GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT

201 AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG

251 GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA

301 ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA

351 ACTGAGATAC CTACAGCGTG AGCATTGAGA AAGCGCCACG CTTCCCGAAG

401 GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG

451 CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT

501 CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG

551 GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCAAGCTA GCTTCTAGCT

601 AGAAATTGTA AACGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTGTT

651 AAATCAGCTC ATTTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT

701 AAATCAAAAG AATAGCCCGA GATAGGGTTG AGTGTTGTTC CAGTTTGGAA

751 CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAAA

801 CCGTCTATCA GGGCGATGGC CGCCCACTAC GTGAACCATC ACCCAAATCA

851 AGTTTTTTGG GGTCGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG

901 GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA

951 AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA

1001 GCGGTCACGC TGCGCGTAAC CACCACACCC GCCGCGCTTA ATGCGCCGCT

1051 ACAGGGCGCG TACTATGGTT GCTTTGACGA GCACGTATAA CGTGCTTTCC

FIG. 6-1

1101 TCGTTGGAAT CAGAGCGGGA GCTAAACAGG AGGCCGATTA AAGGGATTTT

1151 AGACAGGAAC GGTACGCCAG CTGGATCACC GCGGTCTTTC TCAACGTAAC

1201 ACTTTACAGC GGCGCGTCAT TTGATATGAT GCGCCCCGCT TCCCGATAAG

1251 GGAGCAGGCC AGTAAAAGCA TTACCCGTGG TGGGGTTCCC GAGCGGCCAA

1301 AGGGAGCAGA CTCTAAATCT GCCGTCATCG ACTTCGAAGG TTCGAATCCT

1351 TCCCCCACCA CCATCACTTT CAAAAGTCCG AAAGAATCTG CTCCCTGCTT

1401 GTGTGTTGGA GGTCGCTGAG TAGTGCGCGA GTAAAATTTA AGCTACAACA

1451 AGGCAAGGCT TGACCGACAA TTGCATGAAG AATCTGCTTA GGGTTAGGCG

1501 TTTTGCGCTG CTTCGCGATG TACGGGCCAG ATATACGCGT TGACATTGAT

1551 TATTGACTAG TTATTAATAG TAATCAATTA CGGGGTCATT AGTTCATAGC

1601 CCATATATGG AGTTCCGCGT TACATAACTT ACGGTAAATG GCCCGCCTGG

1651 CTGACCGCCC AACGACCCCC GCCCATTGAC GTCAATAATG ACGTATGTTC

1701 CCATAGTAAC GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGACTAT

1751 TTACGGTAAA CTGCCCACTT GGCAGTACAT CAAGTGTATC ATATGCCAAG

1801 TACGCCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCGCC TGGCATTATG

1851 CCCAGTACAT GACCTTATGG GACTTTCCTA CTTGGCAGTA CATCTACGTA

1901 TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG

1951 GCGTGGATAG CGGTTTGACT CACGGGGATT TCCAAGTCTC CACCCCATTG

2001 ACGTCAATGG GAGTTTGTTT TGGCACCAAA ATCAACGGGA CTTTCCAAAA

2051 TGTCGTAACA ACTCCGCCCC ATTGACGCAA ATGGGCGGAA TTCCTGGGCG

2101 GGACTGGGGA GTGGCGAGCC CTCAGATGCT GCATATAAGC AGCTGCTTTT

2151 TGCCTGTACT GGGTCTCTCT GGTTAGACCA GATCTGAGCC TGGGAGCTCT

2201 CTGGCTAACT AGAGAACCCA CTGCTTAAGC CTCAATAAAG CTTCTAGAGA

2251 TCCCTCGACC TCGAGATCCA TTGTGCTGGC GCGGATTCTT TATCACTGAT

FIG. 6-2

2301 AAGTTGGTGG ACATATTATG TTTATCAGTG ATAAAGTGTC AAGCATGACA

2351 AAGTTGCAGC CGAATACAGT GATCCGTGCC GCCCTAGACC TGTTGAACGA

2401 GGTCGGCGTA GACGGTCTGA CGACACGCAA ACTGGCGGAA CGGTTGGGGG

2451 TTCAGCAGCC GGCGCTTTAC TGGCACTTCA GGAACAAGCG GGCGCTGCTC

2501 GACGCACTGG CCGAAGCCAT GCTGGCGGAG AATCATAGCA CTTCGGTGCC

2551 GAGAGCCGAC GACGACTGGC GCTCATTTCT GACTGGGAAT GCCCGCAGCT

2601 TCAGGCAGGC GCTGCTCGCC TACCGCCAGC ACAATGGATC TCGAGGGATC

2651 TTCCATACCT ACCAGTTCTG CGCCTGCAGG TCGCGGCCGC GACTCTAGAG

2701 GATCTTTGTG AAGGAACCTT ACTTCTGTGG TGTGACATAA TTGGACAAAC

2751 TACCTACAGA GATTTAAAGC TCTAAGGTAA ATATAAAATT TTTAAGTGTA

2801 TAATGTGTTA AACTACTGAT TCTAATTGTT TGTGTATTTT AGATTCCAAC

2851 CTATGGAACT GATGAATGGG AGCAGTGGTG GAATGCCTTT AATGAGGAAA

2901 ACCTGTTTTG CTCAGAAGAA ATGCCATCTA GTGATGATGA GGCTACTGCT

2951 GACTCTCAAC ATTCTACTCC TCCAAAAAAG AAGAGAAAGG TAGAAGACCC

3001 CAAGGACTTT CCTTCAGAAT TGCTAAGTTT TTTGAGTCAT GCTGTGTTTA

3051 GTAATAGAAC TCTTGCTTGC TTTGCTATTT ACACCACAAA GGAAAAAGCT

3101 GCACTGCTAT ACAAGAAAAT TATGGAAAAA TATTCTGTAA CCTTTATAAG

3151 TAGGCATAAC AGTTATAATC ATAACATACT GTTTTTTCTT ACTCCACACA

3201 GGCATAGAGT GTCTGCTATT AATAACTATG CTCAAAAATT GTGTACCTTT

3251 AGCTTTTTAA TTTGTAAAGG GGTTAATAAG GAATATTTGA TGTATAGTGC

3301 CTTGACTAGA GATCATAATC AGCCATACCA CATTTGTAGA GGTTTTACTT

3351 GCTTTAAAAA ACCTCCCACA CCTCCCCCTG AACCTGAAAC ATAAAATGAA

3401 TGCAATTGTT GTTGTTAACT TGTTTATTGC AGCTTATAAT GGTTACAAAT

3451 AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTTT TTCACTGCAT

FIG. 6-3

3501 TCTAGTTGTG GTTTGTCCAA ACTCATCAAT GTATCTTATC ATGTCTGGAT

3551 CCTGTGGAAT GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG

3601 CAGGCAGAAG TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT

3651 GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT

3701 CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC

3751 TAACTCCGCC CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT

3801 TTTATTTATG CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA

3851 GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG CTTTTGCAAA AAGCTAATTC

FIG. 6-4

```
     AGACTCTCAGGCCTTGGCAGGTGCGTCTTTCAGTTCCCCTCACACTTCGGGTTCCTCGGG   (60)

     GAGGAGGGGCTGGAACCCTAGCCCATCGTCAGGACAAAGATGCTCAGGCTGCTCTTGGCT   (120)
                                           MetLeuArgLeuLeuLeuAla
                                           -18
     CTCAACTTATTCCCTTCAATTCAAGTAACAGGAAACAAGATTTTGGTGAAGCAGTCGCCC   (180)
     LeuAsnLeuPheProSerIleGlnValThrGlyAsnLysIleLeuValLysGlnSerPro
                                      +1
     ATGCTTGTAGCGTACGACAATGCGGTCAACCTTAGCTGCAAGTATTCCTACAATCTCTTC   (240)
10   MetLeuValAlaTyrAspAsnAlaValAsnLeuSerCysLysTyrSerTyrAsnLeuPhe
                                 ---CHO---
     TCAAGGGAGTTCCGGGCATCCCTTCACAAAGGACTGGATAGTGCTGTGGAAGTCTGTGTT   (300)
30   SerArgGluPheArgAlaSerLeuHisLysGlyLeuAspSerAlaValGluValCysVal

     GTATATGGGAATTACTCCCAGCAGCTTCAGGTTTACTCAAAAACGGGGTTCAACTGTGAT   (360)
50   ValTyrGlyAsnTyrSerGlnGlnLeuGlnValTyrSerLysThrGlyPheAsnCysAsp
            ---CHO---
     GGGAAATTGGGCAATGAATCAGTGACATTCTACCTCCAGAATTTGTATGTTAACCAAACA   (420)
70   GlyLysLeuGlyAsnGluSerValThrPheTyrLeuGlnAsnLeuTyrValAsnGlnThr
              ---CHO---                                  ---CHO---
     GATATTTACTTCTGCAAAATTGAAGTTATGTATCCTCCTCCTTACCTAGACAATGAGAAG   (480)
90   AspIleTyrPheCysLysIleGluValMetTyrProProProTyrLeuAspAsnGluLys

     AGCAATGGAACCATTATCCAT.GTGAAAGGGAAACACCTTTGTCCAAGTCCCCTATTTCCC   (540)
110  SerAsnGlyThrIleIleHisValLysGlyLysHisLeuCysProSerProLeuPhePro
      ---CHO---
     GGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTTGGTGGAGTCCTGGCTTGCTATAGC   (600)
130  GlyProSerLysProPheTrpValLeuValValValGlyGlyValLeuAlaCysTyrSer
                       -----------------------------------TM-------
     TTGCTAGTAACAGTGGCCTTTATTATTTTCTGGGTGAGGAGTAAGAGGAGCAGGCTCCTG   (660)
150  LeuLeuValThrValAlaPheIleIlePheTrpValArgSerLysArgSerArgLeuLeu
     ------------------------------------
     CACAGTGACTACATGAACATGACTCCCCGCCGCCCCGGGCCCACCCGCAAGCATTACCAG   (720)
170  HisSerAspTyrMetAsnMetThrProArgArgProGlyProThrArgLysHisTyrGln

     CCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCTGACACGGACGCCTATCCAGA   (780)
190  ProTyrAlaProProArgAspPheAlaAlaTyrArgSerEnd
                                          202.
     AGCCAGCCGGCTGGCAGCCCCCATCTGCTCAATATCACTGCTCTGGATAGGAAATGACCG   (840)

     CCATCTCCAGCCGGCCACCTCAGCCCCTGTTGGGCCACCAATGCCAATTTTTCTCGAGTG   (900)

     ACTAGACCAAATATCAAGATCATTTTGAGACTCTGAAATGAAGTAAAAGAGATTTCCTGT   (960)

     GACAGGCCAAGTCTTACAGTGCCATGGCCCACATTCCAACTTACCATGTACTTAGTGACT   (1020)

     TGACTGAGAAGTTAGGGTAGAAAACAAAAAGGGAGTGGATTCTGGGAGCCTCTTCCCTTT   (1080)
```

FIG. 7-1

CTCACTCACCTGCACATCTCAGTCAAGCAAAGTGTGGTATCCACAGACATTTTAGTTGCA (1140)

GAAGAAAGGCTAGGAAATCATTCCTTTTGGTTAAATGGGTGTTTAATCTTTTGGTTAGTG (1200)

GGTTAAACGGGGTAAGTTAGAGTAGGGGGAGGGATAGGAAGACATATTTAAAAACCATTA (1260)

AAACACTGTCTCCCACTCATGAAATGAGCCACGTAGTTCCTATTTAATGCTGTTTTCCTT (1320)

TAGTTTAGAAATACATAGACATTGTCTTTTATGAATTCTGATCATATTTAGTCATTTTGA (1380)

CCAAATGAGGGATTTGGTCAAATGAGGGATTCCCTCAAAGCAATATCAGGTAAACCAAGT (1440)

TGCTTTCCTCACTCCCTGTCATGAGACTTCAGTGTTAATGTTCACAATATACTTTCGAAA (1500)

GAATAAAATAGTTC (1514)

FIG. 7-2

TAGACCCAGAGAGGCTCAGCTGCACTCGCCCGGCTGGGAGAGCTGGGTGTGGGGAACATG (60)
MET

GCCGGGCCTCCGAGGCTCCTGCTGCTGCCCCTGCTTCTGGCGCTGGCTCCGCGGCCTGCCT (120)
ALAGLYPROPROARGLEULEULEULEUPROLEULEULEUALALEUALAARGGLYLEUPRO

GGGGCCCTGGCTGCCCAAGGTAAGAGCTTCCCAGGCTCTCCATGGCCACAGCTCCGGAGC (180)
GLYALALEUALAALAGLN /

TCTCCCTGCCCCATGAGCTCAGAGCCCCCAGTCTGAGCCACAGCACAGCCCCCAGGAAGC (240)

GGGTGGGGTGCTGAGCGGCCTCCAGTGTCTGAGGACTCATTTAAGAGAAGGAAAAAGGGT (300)

GGACCCGGTGGGGAGTGGCCGGGGCTGTCCAGGCAGGGCCGCTGCTTTGGGAGGAAGAAG (360)

CCCACAGTCTCGGAACACGAGGACAGCACCTCCCCCAACACCACAGCCGGTGCCCAGATC (420)

TGCTCCATGCCCCGTAAGGCACCGTGTCTTTGGCGACATGTCAGCCCTGGGCTGTCTCAG (480)

GGCCCCACCATCCCCACCACTGTCCCCTGCAGGGAGGACATTCTCTGTCCTTCTGGCCAG (540)
/

ACTGATGGTGACAGCCCAGGTCCTCCCAGAGGTGCAGCAGTCTCCCCACTGCACGACTGT (600)
GLUVALGLNGLNSERPROHISCYSTHRTHRVA

CCCCGTGGGAGCCTCCGTCAACATCACCTGCTCCACCAGCGGGGGCCTGCGTGGGATCTA (660)
LPROVALGLYALASERVALASNILETHRCYSSERTHRSERGLYGLYLEUARGGLYILETY
---CHO---

CCTGAGGCAGCTCGGGCCACAGCCCCAAGACATCATTTACTACGAGGACGGGGTGGTGCC (720)
RLEUARGGLNLEUGLYPROGLNPROGLNASPILEILETYRTYRGLUASPGLYVALVALPR

CACTACGGACAGACGGTTCCGGGGCCGCATCGACTTCTCAGGGTCCCAGGACAACCTGAC (780)
OTHRTHRASPARGARGPHEARGGLYARGILEASPPHESERGLYSERGLNASPASNLEUTH
---CHO--

TATCACCATGCACCGCCTGCAGCTGTCGGACACTGGCACCTACACCTGCCAGGCCATCAC (840)
RILETHRMETHISARGLEUGLNLEUSERASPTHRGLYTHRTYRTHRCYSGLNALAILETH
-

GGAGGTCAATGTCTACGGCTCCGGCACCCTGGTCCTGGTGACAGAGGAACAGTCCCAAGG (900)
RGLUVALASNVALTYRGLYSERGLYTHRLEUVALLEUVALTHRGLUGLUGLNSERGLNGL

ATGGCACAGATGCTCGGACGCCCCACCAAGGGCCTCTGCCCTCCCTGCCCCACCGACAGG (960)
YTRPHISARGCYSSERASPALAPROPROARGALASERALALEUPROALAPROPROTHRGL

CTCCGCCCTCCCTGACCCGCAGACAGCCTCTGCCCTCCCTGACCCGCCAGCAGCCTCTGC (1020)
YSERALALEUPROASPPROGLNTHRALASERALALEUPROASPPROPROALAALASERAL

CCTCCCTGCGGCCCTGGCGGTGATCTCCTTCCTCCTCGGGCTGGGCCTGGGGGTGGCGTG (1080)
ALEUPROALAALALEUALAVALILESERPHELEULEUGLYLEUGLYLEUGLYVALALACY
----------TM----------*

FIG. 8-1

TGTGCTGGCGAGGACACAGATAAAGAAACTGTGCTCGTGGCGGGATAAGAATTCGGCGGC (1140)
SVALLEUALAARGTHRGLNILELYSLYSLEUCYSSERTRPARGASPLYSASNSERALAAL

ATGTGTGGTGTACGAGGACATGTCGCACAGCCGCTGCAACACGCTGTCCTCCCCCAACCA (1200)
ACYSVALVALTYRGLUASPMETSERHISSERARGCYSASNTHRLEUSERSERPROASNGL

GTACCAGTGACCCAGTGGGCCCCTGCACGTCCCGCCTGTGGTCCCCCCAGCACCTTCCCT (1260)
NTYRGLNEND

GCCCCACCATGCCCCCCACCCTGCCACACCCCTCACCCTGCTGTCCTCCCACGGCTGCAG (1320)

CAGAGTTTGAAGGGCCCAGCCGGTGCCCAGCTCCAAGCAGACACACAGGCAGTGGCCAGGC (1380)

CCCACGGTGCTTCTCAGTGGACAATGATGCCTCCTCCGGGAAGCCTTCCCTGCCCAGCCC (1440)

ACGCCGCCACCGGGAGGAAGCCTGACTGTCCTTTGGCTGCATCTCCCGACCATGGCCAAG (1500)

GAGGGCTTTTCTGTGGGATGGGCCTGGCACGCGGCCCTCTCCTGTCAGTGCCGGCCCACC (1560)

CACCAGCAGGCCCCCAACCCCCAGGCAGCCCGGCAGAGGACGGGAGGAGACCAGTCCCCC (1620)

ACCCAGCCGTACCAGAAATAAAGGCTTCTGTGCTTCAAAAAAAAA (1665)

FIG. 8-2

```
    CCCAAATGTCTCAGAATGTATGTCCCAGAAACCTGTGGCTGCTTCAACCATTGACAGTTT   (60)
          METSERGLNASNVALCYSPROARGASNLEUTRPLEULEUGLNPROLEUTHRVALL
      -29
    TGCTGCTGCTGGCTTCTGCAGACAGTCAAGCTGCAGCTCCCCCAAAGGCTGTGCTGAAAC   (120)
    EULEULEULEUALASERALAASPSERGLNALAALAALAPROPROLYSALAVALLEULYSL
                                      -1 +1
    TTGAGCCCCCGTGGATCAACGTGCTCCAGGAGGACTCTGTGACTCTGACATGCCAGGGGG   (180)
10  EUGLUPROPROTRPILEASNVALLEUGLNGLUASPSERVALTHRLEUTHRCYSGLNGLYA
                                                          *
    CTCGCAGCCCTGAGAGCGACTCCATTCAGTGGTTCCACAATGGGAATCTCATTCCCACCC   (240)
30  LAARGSERPROGLUSERASPSERILEGLNTRPPHEHISASNGLYASNLEUILEPROTHRH

    ACACGCAGCCCAGCTACAGGTTCAAGGCCAACAACAATGACAGCGGGGAGTACACGTGCC   (300)
50  ISTHRGLNPROSERTYRARGPHELYSALAASNASNASNASPSERGLYGLUTYRTHRCYSG
                                   ---CHO---                *
    AGACTGGCCAGACCAGCCTCAGCGACCCTGTGCATCTGACTGTGCTTTCCGAATGGCTGG   (360)
70  LNTHRGLYGLNTHRSERLEUSERASPPROVALHISLEUTHRVALLEUSERGLUTRPLEUV

    TGCTCCAGACCCCTCACCTGGAGTTCCAGGAGGGAGAAACCATCATGCTGAGGTGCCACA   (420)
90  ALLEUGLNTHRPROHISLEUGLUPHEGLNGLUGLYGLUTHRILEMETLEUARGCYSHISS
                                                          *
    GCTGGAAGGACAAGCCTCTGGTCAAGGTCACATTCTTCCAGAATGGAAAATCCCAGAAAT   (480)
110 ERTRPLYSASPLYSPROLEUVALLYSVALTHRPHEPHEGLNASNGLYLYSSERGLNLYSP

    TCTCCCGTTTGGATCCCACCTTCTCCATCCCACAAGCAAACCACAGTCACAGTGGTGATT   (540)
130 HESERARGLEUASPPROTHRPHESERILEPROGLNALAASNHISSERHISSERGLYASPT
                                                ---CHO---
    ACCACTGCACAGGAAACATAGGCTACACGCTGTTCTCATCCAAGCCTGTGACCATCACTG   (600)
150 YRHISCYSTHRGLYASNILEGLYTYRTHRLEUPHESERSERLYSPROVALTHRILETHRV
      *
    TCCAAGTGCCCAGCATGGGCAGCTCTTCACCAATGGGGATCATTGTGGCTGTGGTCATTG   (660)
170 ALGLNVALPROSERMETGLYSERSERSERPROMETGLYILEILEVALALAVALVALILEA
                                        ---------------------------
    CGACTGCTGTAGCAGCCATTGTTGCTGCTGTAGTGGCCTTGATCTACTGCAGGAAAAAGC   (720)
190 LATHRALAVALALAALAILEVALALAALAVALVALALALEUILETYRCYSARGLYSLYSA
    ----------TM-----------------------------------*-
    GGATTTCAGCCAATTCCACTGATCCTGTGAAGGCTGCCCAATTTGAGCCACCTGGACGTC   (780)
210 RGILESERALAASNSERTHRASPPROVALLYSALAALAGLNPHEGLUPROPROGLYARGG

    AAATGATTGCCATCAGAAAGAGACAACTTGAAGAAACCAACAATGACTATGAAACAGCTG   (840)
230 LNMETILEALAILEARGLYSARGGLNLEUGLUGLUTHRASNASNASPTYRGLUTHRALAA

    ACGGCGGCTACATGACTCTGAACCCCAGGGCACCTACTGACGATGATAAAAACATCTACC   (900)
250 SPGLYGLYTYRMETTHRLEUASNPROARGALAPROTHRASPASPASPLYSASNILETYRL
```

FIG. 9-1

TGACTCTTCCTCCCAACGACCATGTCAACAGTAATAACTAAAGAGTAACGTTATGCCATG (960)

270 EUTHRLEUPROPROASNASPHISVALASNSERASNASNEND

282

TGGTCATACTCTCAGCTTGCTGAGTGGATGACAAAAAGAGGGGAATTGTTAAAGGAAAAT (1020)

TTAAATGGAGACTGGAAAAATCCTGAGCAAACAAAACCACCTGGCCCTTAGAAATAGCTT (1080)

TAACTTTGCTTAAACTACAAACACAAGCAAAACTTCACGGGGTCATACTACATACAAGCA (1140)

TAAGCAAAACTTAACTTGGATCATTTCTGGTAAATGCTTATGTTAGAAATAAGACAACCC (1200)

CAGCCAATCACAAGCAGCCTACTAACATATAATTAGGTGACTAGGGACTTTCTAAGAAGA (1260)

TACCTACCCCCAAAAAACAATTATGTAATTGAAAACCAACCGATTGCCTTTATTTTGCTT (1320)

CCACATTTTCCCAATAAATACTTGCCTGTGACATTTTGCCACTGGAACACTAAACTTCAT (1380)

GAATTGCGCCTCAGATTTTTCCTTTAACATCTTTTTTTTTTTTTGACAGAGTCTCAATCTG (1440)

TTACCCAGGCTGGAGTGCAGTGGTGCTATCTTGGCTCACTGCAAACCCGCCTCCCAGGTT (1500)

TAAGCGATTCTCATGCCTCAGCCTCCCAGTAGCTGGGATTAGAGGCATGTGCCATCATAC (1560)

CCAGCTAATTTTTTGTATTTTTTATTTTTTTTTTTTTAGTAGAGACAGGGTTTCGCAATGTT (1620)

GGCCAGGCCGATCTCGAACTTCTGGCCTCTAGCGATCTGCCCGCCTCGGCCTCCCAAAGT (1680)

GCTGGGATGACCAGCATCAGCCCCAATGTCCAGCCTCTTTAACATCTTCTTTCCTATGCC (1740)

CTCTCTGTGGATCCCTACTGCTGGTTTCTGCCTTCTCCATGCTGAGAACAAAATCACCTA (1800)

TTCACTGCTTATGCAGTCGGAAGCTCCAGAAGAACAAAGAGCCCAATTACCAGAACCACA (1860)

TTAAGTCTCCATTGTTTTGCCTTGGGATTTGAGAAGAGAATTAGAGAGGTGAGGATCTGG (1920)

TATTTCCTGGACTAAATTCCCCTTGGGGAAGACGAAGGGATGCTGCAGTTCCAAAAGAGA (1980)

AGGACTCTTCCAGAGTCATCTACCTGAGTCCCAAAGCTCCCTGTCCTGAAAGCCACAGAC (2040)

AATATGGTCCCAAATGACTGACTGCACCTTCTGTGCCTCAGCCGTTCTTGACATCAAGAA (2100)

TCTTCTGTTCCACATCCACACAGCCAATACAATTAGTCAAACCACTGTTATTAACAGATG (2160)

TAGCAACATGAGAAACGCTTATGTTACAGGTTACATGAGAGCAATCATGTAAGTCTATAT (2220)

GACTTCAGAAATGTTAAAATAGACTAACCTCTAACAACAAATTAAAAGTGATTGTTTCAA (2280)

GGTGAAAAAA (2290)

FIG. 9-2

```
  1 AAAGACAAACTGCACCCACTGAACTCCGCAGCTAGCATCCAAATCAGCCCTTGAGATTTGAGGCCTTGGAGACTCAGGAGTTTTGAGAGC

 91 AAAATGACAACACCCAGAAATTCAGTAAATGGACTTTCCCGGCAGAGCCAATGAAAGGCCCTATTGCTATGCAATCTGGTCCAAAACCA
  1    MetThrThrProArgAsnSerValAsnGlyThrPheProAlaGluProMetLysGlyProIleAlaMetGlnSerGlyProLysPro
                        ---CHO---

181 CTCTTCAGGAGGATGTCTTCACTGGTGGGCCCCACGCAAAGCTTCTTCATGAGGGAATCTAAGACTTTGGGGGCTGTCCAGATTATGAAT
 30 LeuPheArgArgMetSerSerLeuValGlyProThrGlnSerPhePheMetArgGluSerLysThrLeuGlyAlaValGlnIleMetAsn
                                                                          ===================

271 GGGCTCTTCCACATTGCCCTGGGGGGTCTTCTGATGATCCCAGCAGGGATCTATGCACCCATCTGTGTGACTGTGTGGTACCCTCTCTGG
 60 GlyLeuPheHisIleAlaLeuGlyGlyLeuLeuMetIleProAlaGlyIleTyrAlaProIleCysValThrValTrpTyrProLeuTrp
    ==========================================================================================

361 GGAGGCATTATGTATATTATTTCCGGATCACTCCTGGCAGCAACGGAGAAAAACTCCAGGAAGTGTTTGGTCAAAGGAAAAATGATAATG
 90 GlyGlyIleMetTyrIleIleSerGlySerLeuLeuAlaAlaThrGluLysAsnSerArgLysCysLeuValLysGlyLysMetIleMet
    ==========================================                                     =========

451 AATTCATTGAGCCTCTTTGCTGCCATTTCTGGAATGATTCTTTCAATCATGGACATACTTAATATTAAAATTTCCCATTTTTTAAAAATG
120 AsnSerLeuSerLeuPheAlaAlaIleSerGlyMetIleLeuSerIleMetAspIleLeuAsnIleLysIleSerHisPheLeuLysMet
    ==================================================================

541 GAGAGTCTGAATTTTATTAGAGCTCACACACCATATATTAACATATACAACTGTGAACCAGCTAATCCCTCTGAGAAAAACTCCCCATCT
150 GluSerLeuAsnPheIleArgAlaHisThrProTyrIleAsnIleTyrAsnCysGluProAlaAsnProSerGluLysAsnSerProSer

631 ACCCAATACTGTTACAGCATACAATCTCTGTTCTTGGGCATTTTGTCAGTGATGCTGATCTTTGCCTTCTTCCAGGAACTTGTAATAGCT
180 ThrGlnTyrCysTyrSerIleGlnSerLeuPheLeuGlyIleLeuSerValMetLeuIlePheAlaPhePheGlnGluLeuValIleAla
             ================================================================
```

FIG. 10A-1

```
721  GGCATCGTTGAGAATGAATGGAAAAGAACGTGCTCCAGACCCAAATCTAACATAGTTCTCCTGTCAGCAGAAGAAAAAAAGAACAGACT
210  GlyIleValGluAsnGluTrpLysArgThrCysSerArgProLysSerAsnIleValLeuLeuSerAlaGluGluLysLysGluGlnThr

811  ATTGAAATAAAAGAAGAAGTGGTTGGGCTAACTGAAACATCTTCCCAACCAAAGAATGAAGAAGACATTGAAATTATTCCAATCCAAGAA
240  IleGluIleLysGluGluValValGlyLeuThrGluThrSerSerGlnProLysAsnGluGluAspIleGluIleIleProIleGlnGlu

901  GAGGAAGAAGAAGAAACAGAGACGAACTTTCCAGAACCTCCCCAAGATCAGGAATCCTCACCAATAGAAAATGACAGCTCTCCTTAAGTG
270  GluGluGluGluGluThrGluThrAsnPheProGluProProGlnAspGlnGluSerSerProIleGluAsnAspSerSerProEnd 297
                                                                                  ---CHO---

991  ATTTCTTCTGTTTTCTGTTTCCTTTTTTAAACATTAGTGTTCATAGCTTCCAAGAGACATGCTGACTTTCATTTCTTGAGGTACTCTGCA
                                                      *

1081 CATACGCACCACATCTCTATCTGGCCTTTGCATGGAGTGACCATAGCTCCTTCTCTCTTACATTGAATGTAGAGAATGTAGCCATTGTAG

1171 CAGCTTGTGTTGTCACGCTTCTTCTTTTGAGCAACTTTCTTACACTGAAGAAAGGCAGAATGAGTGCTTCAGAATGTGATTTCCTACTAA

1261 CCTGTTCCTTGGATAGGCTTTTTAGTATAGTATTTTTTTTTGTCATTTTCTCCATCAGCAACCAGGGAGACTGCACCTGATGGAAAAGAT

1351 ATATGACTGCTTCATGACATTCCTAAACTATCTTTTTTTTATTCCACATCTACGTTTTTGGTGGAGTCCCTTTTTATCATCCTTAAAACA

1441 ATGATGCAAAAGGGCTTTAGAGCACAATGGATCT 1474
```

FIG. 10A-2

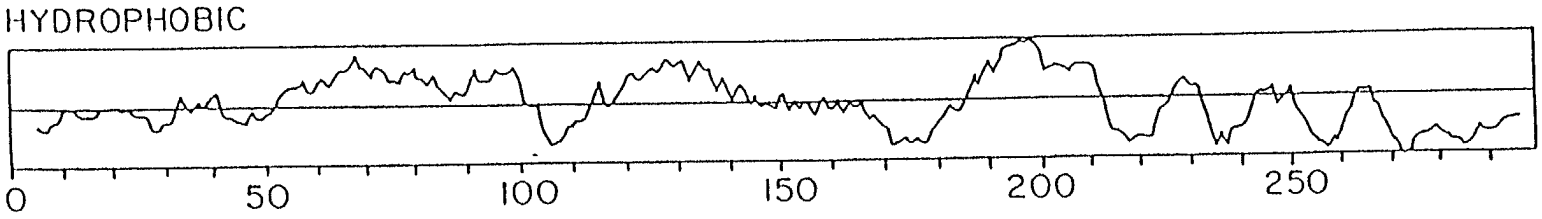


FIG. 10B

```
1    CTCAGCCTCGCTATGGCTCCCAGCAGCCCCCGGCCCGCGCTGCCCGCACTCCTGGTCCTGCTCGGGGCTCTGTTCCCA
                 MetAlaProSerSerProArgProAlaLeuProAlaLeuLeuValLeuLeuGlyAlaLeuPhePro
                (-25)
     GGACCTGGCAATGCCCAGACATCTGTGTCCCCCTCAAAAGTC
     GlyProGlyAsnAlaGlnThrSerValSerProSerLysVal
            (+1)                         (+11)
121  ATCCTGCCCCGGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCAGCCCAAGTTGTTGGGCATAGAGACC
     IleLeuProArgGlyGlySerValLeuValThrCysSerThrSerCysAspGlnProLysLeuLeuGlyIleGluThr

     CCGTTGCCTAAAAAGGAGTTGCTCCTGCCTGGGAACAACCGG
     ProLeuProLysLysGluLeuLeuLeuProGlyAsnAsnArg
                                          (+61)
241  AAGGTGTATGAACTGAGCAATGTGCAAGAAGATAGCCAACCAATGTGCTATTCAAACTGCCCTGATGGGCAGTCAACA
     LysValTyrGluLeuSerAsnValGlnGluAspSerGlnProMetCysTyrSerAsnCysProAspGlyGlnSerThr

     GCTAAAACCTTCCTCACCGTGTACTGGACTCCAGAACGGGTG
     AlaLysThrPheLeuThrValTyrTrpThrProGluArgVal
                                          (+91)
361  GAACTGGCACCCCTCCCCTCTTGGCAGCCAGTGGGCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGGCACCC
     GluLeuAlaProLeuProSerTrpGlnProValGlyLysAsnLeuThrLeuArgCysGlnValGluGlyGlyAlaPro
                                         ---CHO---
     CGGGCCAACCTCACCGTGGTGCTGCTCCGTGGGGAGAAGGAG
     ArgAlaAsnLeuThrValValLeuLeuArgGlyGluLysGlu
                              ----------(+131)
481  CTGAAACGGGAGCCAGCTGTGGGGGAGCCCGCTGAGGTCACGACCACGGTGCTGGTGAGGAGAGATCACCATGGAGCC
     LeuLysArgGluProAlaValGlyGluProAlaGluValThrThrThrValLeuValArgArgAspHisHisGlyAla

     AATTTCTCGTGCCGCACTGAACTGGACCTGCGGCCCCAAGGG
     AsnPheSerCysArgThrGluLeuAspLeuArgProGlnGly
     ---CHO---                            (+171)
601  CTGGAGCTGTTTGAGAACACCTCGGCCCCCTACCAGCTCCAGACCTTTGTCCTGCCAGCGACTCCCCCACAACTTGTC
     LeuGluLeuPheGluAsnThrSerAlaProTyrGlnLeuGlnThrPheValLeuProAlaThrProProGlnLeuVal
                ---CHO---
     AGCCCCCGGGTCCTAGAGGTGGACACGCAGGGGACCGTGGTC
     SerProArgValLeuGluValAspThrGlnGlyThrValVal
                                          (+211)
```

FIG. 11-1

```
721  TGTTCCCTGGACGGGCTGTTCCCAGTCTCGGAGGCCCAGGTCCACCTGGCACTGGGGGACCAGAGGTTGAACCCCACA
     CysSerLeuAspGlyLeuPheProValSerGluAlaGlnValHisLeuAlaLeuGlyAspGlnArgLeuAsnProThr

     GTCACCTATGGCAACGACTCCTTCTCGGCCAAGGCCTCAGTC
     ValThrTyrGlyAsnAspSerPheSerAlaLysAlaSerVal
                  ---CHO---                (+251)

841  AGTGTGACCGCAGAGGACGAGGGCACCCAGCGGCTGACGTGTGCAGTAATACTGGGGAACCAGAGCCAGGAGACACTG
     SerValThrAlaGluAspGluGlyThrGlnArgLeuThrCysAlaValIleLeuGlyAsnGlnSerGlnGluThrLeu
                                                          ---CHO---

     CAGACAGTGACCATCTACAGCTTTCCGGCGCCCAACGTGATT
     GlnThrValThrIleTyrSerPheProAlaProAsnValIle
                                        (+291)

961  CTGACGAAGCCAGAGGTCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGGCCCACCCTAGAGCCAAGGTGACGCTG
     LeuThrLysProGluValSerGluGlyThrGluValThrValLysCysGluAlaHisProArgAlaLysValThrLeu

     AATGGGGTTCCAGCCCAGCCACTGGGCCCGAGGGCCCAGCTC
     AsnGlyValProAlaGlnProLeuGlyProArgAlaGlnLeu
                                        (+331)

1081 CTGCTGAAGGCCACCCCAGAGGACAACGGGCGCAGCTTCTCCTGCTCTGCAACCCTGGAGGTGGCCGGCCAGCTTATA
     LeuLeuLysAlaThrProGluAspAsnGlyArgSerPheSerCysSerAlaThrLeuGluValAlaGlyGlnLeuIle

     CACAAGAACCAGACCCGGGAGCTTCGTGTCCTGTATGGCCCC
     HisLysAsnGlnThrArgGluLeuArgValLeuTyrGlyPro
          ---CHO---                     (+371)

1201 CGACTGGACGAGAGGGATTGTCCGGGAAACTGGACGTGGCCAGAAAATTCCCAGCAGACTCCAATGTGCCAGGCTTGG
     ArgLeuAspGluArgAspCysProGlyAsnTrpThrTrpProGluAsnSerGlnGlnThrProMetCysGlnAlaTrp
                                   ---CHO---

     GGGAACCCATTGCCCGAGCTCAAGTGTCTAAAGGATGGCACT
     GlyAsnProLeuProGluLeuLysCysLeuLysAspGlyThr
                                        (+411)

1321 TTCCCACTGCCCATCGGGGAATCAGTGACTGTCACTCGAGATCTTGAGGGCACCTACCTCTGTCGGGCCAGGAGCACT
     PheProLeuProIleGlyGluSerValThrValThrArgAspLeuGluGlyThrTyrLeuCysArgAlaArgSerThr

     CAAGGGGAGGTCACCCGCGAGGTGACCGTGAATGTGCTCTCC
     GlnGlyGluValThrArgGluValThrValAsnValLeuSer
                                        (+451)
```

FIG. 11-2

```
1441 CCCCGGTATGAGATTGTCATCATCACTGTGGTAGCAGCCGCAGTCATAATGGGCACTGCAGGCCTCAGCACGTACCTC
     ProArgTyrGluIleValIleIleThrValValAlaAlaAlaValIleMetGlyThrAlaGlyLeuSerThrTyrLeu
                     ------------------------------------TM--------------------------------

     TATAACCGCCAGCGGAAGATCAAGAAATACAGACTACAACAG
     TyrAsnArgGlnArgLysIleLysLysTyrArgLeuGlnGln
                                         (+491)
     ---
1561 GCCCAAAAAGGGACCCCCATGAAACCGAACACACAAGCCACGCCTCCCTGAACCTATCCCGGGACAGGGCCTCTTCCT
     AlaGlnLysGlyThrProMetLysProAsnThrGlnAlaThrProPro
                                               (+507)

     CGGCCTTCCCATATTGGTGGCAGTGGTGCCACACTGAACAGA


1681 GTGGAAGACATATGCCATGCAGCTACACCTACCGGCCCTGGGACGCCGGAGGACAGGGCATTGTCCTCAGTCAGATAC
1801 GGCCACGCATCTGATCTGTAGTCACATGACTAAGCCAAGAGGAAGG
     AACAGCATTTGGGGCCATGGTACCTGCACACCTAAAACACTA
```

FIG. 11-3

```
   1  ..GGAGAGTC TGACCACCAT GCCACCTCCT CGCCTCCTCT TCTTCCTCCT
  51  CTTCCTCACC CCCATGGAAG TCAGGCCCGA GGAACCTCTA GTGGTGAAGG
 101  TGGAAGAGGG AGATAACGCT GTGCTGCAGT GCCTCAAGGG GACCTCAGAT
 151  GGCCCCACTC AGCAGCTGAC CTGGTCTCGG GAGTCCCCGC TTAAACCCTT
 201  CTTAAAACTC AGCCTGGGGC TGCCAGGCCT GGGAATCCAC ATGAGGCCCC
 251  TGGcCATCTG GCTTTTCATC TTCAACGTCT CTCAACAGAT GGGGGGCTTC
 301  TACCTGTGCC AGCCGGGGCC CCCCTCTGAG AAGGCCTGGC AGCCTGGCTG
 351  GACAGTCAAT GTGGAGGGCA GCGGGGAGCT GTTCCGGTGG AATGTTTCGG
 401  ACCTAGGTGG CCTGGGCTGT GGCCTGAAGA ACAGGTCCTC AGAGGGCCCC
 451  AGCTCCCCTT CCGGGAAGCT CATGAGCCCC AAGCTGTATG TGTGGGCCAA
 501  AGACCGCCCT GAGATCTGGG AGGGAGAGCC TCCGTGTGTC CCACCGAGGG
 551  ACAGCCTGAA CCAGAGCCTC AGCCAGGACC TCACCATGGC CCCTGGCTCC
 601  ACACTCTGGC TGTCCTGTGG GGTACCCCCT GACTCTGTGT CCAGGGGCCC
 651  CCTCTCCTGG ACCCATGTGC ACCCCAAGGG GCCTAAGTCA TTGCTGAGCC
 701  TAGAGCTGAA GGACGATCGC CCGGCCAGAG ATATGTGGGT AATGGAGACG
 751  GGTCTGTTGT TGCCCCGGGC CACAGCTCAA GACGCTGGAA AGTATTATTG
 801  TCACCGTGGC AACCTGACCA TGTCATTCCA CCTGGAGATC ACTGCTCGGC
 851  CAGTACTATG GCACTGGCTG CTGAGGACTG GTGGCTGGAA GGTCTCAGCT
 901  GTGACTTTGG CTTATCTGAT CTTCTGCCTG TGTTCCCTTG TGGGCATTCT
 951  TCATCTTCAA AGAGCCCTGG TCCTGAGGAG GAAAAGAAAG CGAATGACTG
1001  ACCCCACCAG GAGATTCTTC AAAGTGACGC CTCCCCCAGG AAGCGGGCCC
1051  CAGAACCAGT ACGGGAACGT GCTGTCTCTC CCCACACCCA CCTCAGGCCT
1101  CGGACGCGCC CAGCGTTGGG CCGCAGGCCT GGGGGGCACT GCCCCGTCTT
1151  ATGGAAACCC GAGCAGCGAC GTCCAGGCGG ATGGAGCCTT GGGGTCCCGG
```

FIG. 12–1

1201 AGCCGCCGGG AGTGGGCCCA GAAGAAGAGG AAGGGGAGGG CTATGAGGAA

1251 CCTGACAGTG AGGAGGACTC CGAGTTCTAT GAGAACGACT CCAACCTTGG

1301 GCAGGACCAG CTCTCCCAGG ATGGCAGCGG CTACGAGAAC CCTGAGGATG

1351 AGCCCCTGGG TCCTGAGGAT GAAGACTCCT TCTCCAACGC TGAGTCTTAT

1401 GAGAACGAGG ATGAAGAGCT GACCCAGCCG GTCGCCAGGA CAATGGACTT

1451 CCTGAGCCCT CATGGGTCAG CCTGGGACCC CAGCCGGGAA GCAACCTCCC

1501 TGGGGTCCCA GTCCTATGAG GATATGAGAG GAATCCTGTA TGCAGCCCCC

1551 CAGCTCCGCT CCATTCGGGG CCAGCCTGGA CCCAATCATG AGGAAGATGC

1601 AGACTCTTAT GAGAACATGG ATAATCCCGA TGGGCCAGAC CCAGCCTGGG

1651 GAGGAGGGGG CCGCATGGGC ACCTGGAGCA CCAGGTGATC CTCAGGTGGC

1701 CAGCCTGGAT CTCCTCAAGT CCCCAAGATT CACACCTGAC TCTGAAATCT

1751 GAAGACCTCG AGCAGATGAT GCCAACCTCT GGAGCAATGT TGCTTAGGAT

1801 GTGTGCATGT GTGTAAGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT

1851 ATACATGCCA GTGACACTTC CAGTCCCCTT TGTATTCCTT AAATAAACTC

1901 AATGAGCTCT TCCAAAAAAA AAAA

FIG. 12-2

1 ACAAAGACAA ACTGCACCCA CTGAACTCCG CAGCTAGCAT CCAAATCAGC
51 CCTTGAGATT TGAGGCCTTG GAGACTCAGG AGTTTTGAGA GCAAAATGAC
101 AACACCCAGA AATTCAGTAA ATGGGACTTT CCCGGCAGAG CCAATGAAAG
151 GCCCTATTGC TATGCAATCT GGTCCAAAAC CACTCTTCAG GAGGATGTCT
201 TCACTGGTGG GCCCCACGCA AAGCTTCTTC ATGAGGGAAT CTAAGACTTT
251 GGGGGCTGTC CAGATTATGA ATGGGCTCTT CCACATTGCC CTGGGGGGTC
301 TTCTGATGAT CCCAGCAGGG ATCTATGCAC CCATCTGTGT GACTGTGTGG
351 TACCCTCTCT GGGGAGGCAT TATGTATATT ATTTCCGGAT CACTCCTGGC
401 AGCAACGGAG AAAAACTCCA GGAAGTGTTT GGTCAAAGGA AAAATGATAA
451 TGAATTCATT GAGCCTCTTT GCTGCCATTT CTGGAATGAT TCTTTCAATC
501 ATGGACATAC TTAATATTAA AATTTCCCAT TTTTTAAAAA TGGAGAGTCT
551 GAATTTTATT AGAGCTCACA CACCATATAT TAACATATAC AACTGTGAAC
601 CAGCTAATCC CTCTGAGAAA AACTCCCCAT CTACCCAATA CTGTTACAGC
651 ATACAATCTC TGTTCTTGGG CATTTTGTCA GTGATGCTGA TCTTTGCCTT
701 CTTCCAGGAA CTTGTAATAG CTGGCATCGT TGAGAATGAA TGGAAAAGAA
751 CGTGCTCCAG ACCCAAATCT AACATAGTTC TCCTGTCAGC ACAAGAAAAA
801 AAAGAACAGA CTATTGAAAT AAAAGAAGAA GTGGTTGGGC TAACTGAAAC
851 ATCTTCCCAA CCAAAGAATG AAGAAGACAT TGAAATTATT CCAATCCAAG
901 AAGAGGAAGA AGAAGAAACA GAGACGAACT TTCCAGAACC TCCCCAAGAT
951 CAGGAATCCT CACCAATAGA AAATGACAGC TCTCCTTAAG TGATTTCTTC
1001 TGTTTTCTGT TTCCTTTTTT AAACATTAGT GTTCATAGCT TCCAAGAGAC
1051 ATGCTGACTT TCATTTCTTG AGGTACTCTG CACATACGCA CCACATCTCT

FIG. 13-1

1101 ATCTGGCCTT TGCATGGAGT GACCATAGCT CCTTCTCTCT TACATTGAAT

1151 GTAGAGAATG TAGCCATTGT AGCAGCTTGT GTTGTCACGC TTCTTCTTTT

1201 GAGCAACTTT CTTACACTGA AGAAAGGCAG AATGAGTGCT TCAGAATGTG

1251 ATTTCCTACT AACCTGTTCC TTGGATAGGC TTTTTAGTAT AGTATTTTTT

1301 TTTGTCATTT TCTCCATCAG CAACCAGGGA GACTGCACCT GATGGAAAAG

1351 ATATATGACT GCTTCATGAC ATTCCTAAAC TATCTTTTTT TTATTCCACA

1401 TCTACGTTTT TGGTGGAGTC CCTTTTTATC ATCCTTAAAA CAATGATGCA

1451 AAAGGGCTTT AGAGCACAAT GGATCT

FIG. 13-2

```
   1  CCCAAATGTC TCAGAATGTA TGTCCCAGAA ACCTGTGGCT GCTTCAACCA
  51  TTGACAGTTT TGCTGCTGCT GGCTTCTGCA GACAGTCAAG CTGCAGCTCC
 101  CCCAAAGGCT GTGCTGAAAC TTGAGCCCCC GTGGATCAAC GTGCTCCAGG
 151  AGGACTCTGT GACTCTGACA TGCCAGGGGG CTCGCAGCCC TGAGAGCGAC
 201  TCCATTCAGT GGTTCCACAA TGGGAATCTC ATTCCCACCC ACACGCAGCC
 251  CAGCTACAGG TTCAAGGCCA ACAACAATGA CAGCGGGGAG TACACGTGCC
 301  AGACTGGCCA GACCAGCCTC AGCGACCCTG TGCATCTGAC TGTGCTTTCC
 351  GAATGGCTGG TGCTCCAGAC CCCTCACCTG GAGTTCCAGG AGGGAGAAAC
 401  CATCATGCTG AGGTGCCACA GCTGGAAGGA CAAGCCTCTG GTCAAGGTCA
 451  CATTCTTCCA GAATGGAAAA TCCCAGAAAT TCTCCCGTTT GGATCCCACC
 501  TTCTCCATCC CACAAGCAAA CCACAGTCAC AGTGGTGATT ACCACTGCAC
 551  AGGAAACATA GGCTACACGC TGTTCTCATC CAAGCCTGTG ACCATCACTG
 601  TCCAAGTGCC CAGCATGGGC AGCTCTTCAC CAATGGGGAT CATTGTGGCT
 651  GTGGTCATTG CGACTGCTGT AGCAGCCATT GTTGCTGCTG TAGTGGCCTT
 701  GATCTACTGC AGGAAAAAGC GGATTTCAGC CAATTCCACT GATCCTGTGA
 751  AGGCTGCCCA ATTTGAGCCA CCTGGACGTC AAATGATTGC CATCAGAAAG
 801  AGACAACTTG AAGAAACCAA CAATGACTAT GAAACAGCTG ACGGCGGCTA
 851  CATGACTCTG AACCCCAGGG CACCTACTGA CGATGATAAA AACATCTACC
 901  TGACTCTTCC TCCCAACGAC CATGTCAACA GTAATAACTA AAGAGTAACG
 951  TTATGCCATG TGGTCATACT CTCAGCTTGC TGAGTGGATG ACAAAAAGAG
1001  GGGAATTGTT AAAGGAAAAT TTAAATGGAG ACTGGAAAAA TCCTGAGCAA
1051  ACAAAACCAC CTGGCCCTTA GAAATAGCTT TAACTTTGCT TAAACTACAA
1101  ACACAAGCAA AACTTCACGG GGTCATACTA CATACAAGCA TAAGCAAAAC
1151  TTAACTTGGA TCATTTCTGG TAAATGCTTA TGTTAGAAAT AAGACAACCC
1201  CAGCCAATCA CAAGCAGCCT ACTAACATAT AATTAGGTGA CTAGGGACTT
1251  TCTAAGAAGA TACCTACCCC CAAAAAACAA TTATGTAATT GAAAACCAAC
1301  CGATTGCCTT TATTTTGCTT CCACATTTTC CCAATAAATA CTTGCCTGTG
1351  ACATTTTGCC ACTGGAACAC TAAACTTCAT GAATTGCGCC TCAGATTTTT
1401  CCTTTAACAT CTTTTTTTTT TTTGACAGAG TCTCAATCTG TTACCCAGGC
1451  TGGAGTGCAG TGGTGCTATC TTGGCTCACT GCAAACCCGC CTCCCAGGTT
1501  TAAGCGATTC TCATGCCTCA GCCTCCCAGT AGCTGGGATT AGAGGCATGT
1551  GCCATCATAC CCAGCTAATT TTTGTATTTT TTATTTTTTT TTTTTAGTAG
1601  AGACAGGGTT TCGCAATGTT GGCCAGGCCG ATCTCGAACT TCTGGCCTCT
1651  AGCGATCTGC CCGCCTCGGC CTCCCAAAGT GCTGGGATGA CCAGCATCAG
```

FIG. 15-1

1701 CCCCAATGTC CAGCCTCTTT AACATCTTCT TTCCTATGCC CTCTCTGTGG
1751 ATCCCTACTG CTGGTTTCTG CCTTCTCCAT GCTGAGAACA AAATCACCTA
1801 TTCACTGCTT ATGCAGTCGG AAGCTCCAGA AGAACAAAGA GCCCAATTAC
1851 CAGAACCACA TTAAGTCTCC ATTGTTTTGC CTTGGGATTT GAGAAGAGAA
1901 TTAGAGAGGT GAGGATCTGG TATTTCCTGG ACTAAATTCC CCTTGGGGAA
1951 GACGAAGGGA TGCTGCAGTT CCAAAAGAGA AGGACTCTTC CAGAGTCATC
2001 TACCTGAGTC CCAAAGCTCC CTGTCCTGAA AGCCACAGAC AATATGGTCC
2051 CAAATGACTG ACTGCACCTT CTGTGCCTCA GCCGTTCTTG ACATCAAGAA
2101 TCTTCTGTTC CACATCCACA CAGCCAATAC AATTAGTCAA ACCACTGTTA
2151 TTAACAGATG TAGCAACATG AGAAACGCTT ATGTTACAGG TTACATGAGA
2201 GCAATCATGT AAGTCTATAT GACTTCAGAA ATGTTAAAAT AGACTAACCT
2251 CTAACAACAA ATTAAAAGTG ATTGTTTCAA GGTGAAAAAA

FIG. 15-2

```
   1  GCTGTGACTG CTGTGCTCTG GGCGCCACTC GCTCCAGGGA GTGATGGGAA
  51  TCCTGTCATT CTTACCTGTC CTTGCCACTG AGAGTGACTG GGCTGACTGC
 101  AAGTCCCCCC AGCCTTGGGG TCATATGCTT CTGTGGACAG CTGTGCTATC
 151  CCTGGCTCCT GTTGCTGGGA CACCTGCAGC TCCCCCAAAG GCTGTGCTGA
 201  AACTCGAGCC CCAGTGGATC AACGTGCTCC AGGAGGACTC TGTGACTCTG
 251  ACATGCCGGG GGACTCACAG CCCTGAGAGC GACTCCATTC AGTGGTTCCA
 301  CAATGGGAAT CTCATTCCCA CCCACACGCA GCCCAGCTAC AGGTTCAAGG
 351  CCAACAACAA TGACAGCGGG GAGTACACGT GCCAGACTGG CCAGACCAGC
 401  CTCAGCGACC CTGTGCATCT GACTGTGCTT TCTGGTCAGT GGAGGAAGGC
 451  CCCAGGGTGG ACCTGGGAGG GCCAGGACGG ATGAAATCTG CTTTCAGGCA
 501  GAGGTTTGCA GGAAAGGGGG GTGGCCTGCT TACTGGGAAG TATCGCTGTG
 551  AGTTGCCTCA GCACATATCA GTGGTTGTTT TTGCCTCAGT TCTGATTGAA
 601  CAGAAGAAGG TTTCAAGGCC AAAAACAGGC AGCCAAGTGT GAGAGAAGCA
 651  GAAGGAAATC CCTACTGCAT AAAACCCATT TCCATTTTAA TGGCAGAATT
 701  GAAAAGCACA GACCACAACT GAATCCTAGC CCTGGAAATG ACTCACTATA
 751  CAACATGATG AATTCATTTA ACCCTTGAGT TTCCATTTCT TCACCTGCTC
 801  CGTGGGGCAG TAACGCCTCC CTCAGAGGCT TCTGGTGAGA ATCAGTGTTT
 851  CCCTGCCCCC GCCCCGCCCT CCATGCCCCT TCTCCACGTT CTCACTGTGC
 901  TAGGTGCTCT TCTCTGTCTT TCTCTTCCAC CAGCCTGTGG GAAACCTGAG
 951  ATGAAAGTCG TGTCTTACCC ATCTTTGTAT TTCCAGCATC TGAAACTGGG
1001  CAGAGCTTAA TAAATATTTT GCTGGAGAGG TTGATGATCT TACAAAGCTC
1051  CCATTGAAAG GTGGCTCTCT GTAAAGCAAA GTTACAATGA GATTGTGATG
1101  AACATTGTCC TTGTGGCTTT TCACTTAGTC CCCTCCCTTC ACCTGAAGAG
1151  CAAATTTTCC TCAAAAGTAC ACAGCAAACG AATGACCCAC TGGTGACACT
1201  GTTGCCTTTA GACCCTGCTG GAAAGAAGCT CCACATTTAT TAACATTCCC
1251  GAAGTAAATT TATCAGGTAG CATTCATCAG GTAACATTTG TTGCACATTC
1301  ATGACTTTTC TACTGTCCAC AAAGGCATAT GTCCTTATCA TATGCGGACT
1351  CCTCGGTCAC ACTGGATTCT TCCTTCCCTC CTCGACATGG AAGAGATGGC
1401  ATCTTAGGGT CTCTTGTGTT CTTCCTGCAG AGGCCTGTCG GGCAGGAAAA
1451  GGCTGCAGCT GCCTTCCTGG GAGAAGGAGG AGATGAGTGT ATCCTGAACA
1501  CCTATTATGT GCTAGGGGCT ATTGTAGATA CATGACACTA TCATGCTCAT
1551  TTTCACGAAT GAGGAAACTG AGGCTCAGAA GACTTAAATT ATTTGCCCAA
1601  GAGTTATAAA TGACAGAGCC AGCATTAGAG TCCAGGACTG TCTGATTTCA
1651  GACCTAAGCT GTTCCCTCTG CACATCGTGT CCCACCAGTA AGGAAGATCT
```

FIG. 16-1

1701 GGGTCTCAGA GCTGAGCCAA GACCTCCCGG GTCCTCTGCG GTTTTTTGTG
1751 TCTTTCAGAG TGGCTGGTGC TCCAGACCCC TCACCTGGAG TTCCAGGAGG
1801 GAGAAACCAT CGTGCTGAGG TGCCACAGCT GGAAGGACAA GCCTCTGGTC
1851 AAGGTCACAT TCTTCCAGAA TGGAAAATCC AAGAAATTTT CCCGTTCGGA
1901 TCCCAACTTC TCCATCCCAC AAGCAAACCA CAGTCACAGT GGTGATTACC
1951 ACTGCACAGG AAACATAGGC TACACGCTGT ACTCATCCAA GCCTGTGACC
2001 ATCACTGTCC AAGCTCCCAG CTCTTCACCG ATGGGGATCA TTGTGGCTGT
2051 GGTCACTGGG ATTGCTGTAG CGGCCATTGT TGCTGCTGTA GTGGCCTTGA
2101 TCTACTGCAG GAAAAAGCGG ATTTCAGGTT TGTAGCTCCT CCCGGTCCCT
2151 TTTGTTATCA GTTTCCACTT T

FIG. 16-2

```
   1  GCCTCGCTCG GGCGCCCAGT GGTCCTGCCG CCTGGTCTCA CCTCGCCATG
  51  GTTCGTCTGC CTCTGCAGTG CGTCCTCTGG GGCTGCTTGC TGACCGCTGT
 101  CCATCCAGAA CCACCCACTG CATGCAGAGA AAAACAGTAC CTAATAAACA
 151  GTCAGTGCTG TTCTTTGTGC CAGCCAGGAC AGAAACTGGT GAGTGACTGC
 201  ACAGAGTTCA CTGAAACGGA ATGCCTTCCT TGCGGTGAAA GCGAATTCCT
 251  AGACACCTGG AACAGAGAGA CACACTGCCA CCAGCACAAA TACTGCGACC
 301  CCAACCTAGG GCTTCGGGTC CAGCAGAAGG GCACCTCAGA AACAGACACC
 351  ATCTGCACCT GTGAAGAAGG CTGGCACTGT ACGAGTGAGG CCTGTGAGAG
 401  CTGTGTCCTG CACCGCTCAT GCTCGCCCGG CTTTGGGGTC AAGCAGATTG
 451  CTACAGGGGT TTCTGATACC ATCTGCGAGC CCTGCCCAGT CGGCTTCTTC
 501  TCCAATGTGT CATCTGCTTT CGAAAAATGT CACCCTTGGA CAAGCTGTGA
 551  GACCAAAGAC CTGGTTGTGC AACAGGCAGGC ACAAACAAGA CTGATGTTGT
 601  CTGTGGTCCC CAGGATCGGC TGAGAGCCCT GGTGGTGATC CCCATCATCT
 651  TCGGGATCCT GTTTGCCATC CTCTTGGTGC TGGTCTTTAT CAAAAAGGTG
 701  GCCAAGAAGC CAACCAATAA GGCCCCCCAC CCCAAGCAGG AACCCCAGGA
 751  GATCAATTTT CCCGACGATC TTCCTGGCTC CAACACTGCT GCTCCAGTGC
 801  AGGAGACTTT ACATGGATGC CAACCGGTCA CCCAGGAGGA TGGCAAAGAG
 851  AGTCGCATCT CAGTGCAGGA GAGACAGTGA GGCTGCACCC ACCCAGGAGT
 901  GTGGCCACGT GGGCAAACAG GCAGTTGGCC AGAGAGCCTG GTGCTGCTGC
 951  TGCAGGGGTG CAGGCAGAAG CGGGGAGCTA TGCCCAGTCA GTGCCAGCCC
      CTC
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FIG. 17